Amendments to the Specification:

Please replace the paragraph beginning at page 1, line 8, with the following amended paragraph:

This application is a continuation of U.S. Application No. 10/061,943, filed February 1, 2002, which claims the benefit of U.S. Provisional Application No. 60/265,925, filed February 2, 2001, both of which ~~is~~ are incorporated herein by reference in ~~its~~ their entirety for all purposes.

Please replace the paragraph beginning at page 19, line 1, with the following amended paragraph:

3.2.3 CMV UL146 (vCXC1): CMV UL146 encodes a CXC (alpha) chemokine homolog found in human CMV strains. Certain of the inventors have also demonstrated that a UL146 homolog exists in rhesus CMV. vCXC1 shows high inter-strain variability in amino acid sequence, but has conserved structural features, including the ELRCXC (SEQ ID NO:10) motif conserved in all clinical strains sequence to date. The protein encoded by the Toledo strain UL146 has been demonstrated to have neutrophil chemo-attractant properties and acts through the CXCR2 receptor (Penfold et al., 1999, *Proc Natl Acad Sci USA* 96:9839-44). Thus, the vCXC1 polypeptide appears to play a role in neutrophil-mediated dissemination of CMV.

Please replace the paragraph beginning at page 34, line 27, with the following amended paragraph:

Using viral DNA extracted from human CMV strain AD169 (Genbank Accession no. x17403) virions as template, PCR amplification is carried out using the primers: gtgaattcggttggttccccgtgttt (SEQ ID NO:11) (AD27up) and gcggatcctcgcgagtcgcgtcttcatcgtag (SEQ ID NO:12) (AD28low) to amplify AD27/28. The resulting 822 bp fragment is purified, digested with *Bam*HI and *Eco*RI, and cloned into *Bam*HI and *Eco*RI digested vector (pGEM3 (Promega)). The resulting construct is called pGEM28.1.

Please replace the paragraph beginning at page 34, line 33, with the following amended paragraph:

Using the same viral DNA template as above, PCR amplification is carried out using the primers: gtggatcctcgagcgctcgccttttgtcact (SEQ ID NO:13) (AD28up) and gcggatccccccgccc accatacaac (SEQ ID NO:14) (AD29low) to amplify AD27/28. The resulting 877 bp fragment is purified, digested with *Bam*HI, cloned into pGEM28.1, cut with *Bam*HI with the end homologous to AD28up juxtaposed to sequence homologous to AD28low. The resulting construct is called pGEM28.2.

Please replace the paragraph beginning at page 35, line 5, with the following amended paragraph:

To clone the human CCR7 receptor (CCR7 mRNA sequence, Genbank Accession no. XM 049959), whole cell RNA is isolated from human PBMC (e.g. using commercially available kits, Qiagen, CA). PCR amplification is carried out using the primers: gcgaattcagcgtcatggacctgggg (SEQ ID NO:15) (ccr7up) and tggaattcagaagagtcgcctatggg (SEQ ID NO:16) (ccr7low) to amplify CCR7.1. The resulting 1172 bp product is purified, digested with *Eco*RI, and cloned into pIRESpuro (Clontech) at the *EcoR*I site. The resulting construct is called pIRES CCR7.1.

Please replace the paragraph beginning at page 35, line 31, with the following amended paragraph:

Using viral DNA extracted from murine CMV (e.g., strain Smith (Genbank Accession no. U68299)) virions as template, PCR amplification is carried out using the primers: ataagaatgcggccgctcgactacatgctgctgc (SEQ ID NO:17) (S78.1) and cggaattccgtccggctgctgcgcttcttc (SEQ ID NO:18) (S78.2). The 2351bp PCR fragment is isolated and digested with *Not*I and

*Eco*RI, and cloned into *Not*I and *Eco*RI digested vector (pGEM11 (Promega)). The resulting construct is called pGEMm78.

Please replace the paragraph beginning at page 36, line 3, with the following amended paragraph:

To clone the murine CCR7 receptor (mCCR7 mRNA sequence, Genbank Accession no. NM_007719), murine genomic DNA is isolated from murine PBMC (e.g. using commercially available kits, Qiagen, CA). PCR amplification is carried out using the primers: ataagaatgcggccgctgacccagggaaacccagg (SEQ ID NO:19) (mCCR7up) and cggaattccgtcagctcctgggagaggtccttg (SEQ ID NO:20) (mCCR7low) to amplify mCCR7. This fragment is digested with *Not*I and *Eco*RI and cloned into *Not*I and *Eco*RI digested pIRESpuro (Clontech) to give pIRESpuromCCR7. The pIRESpuromCCR7 vector construct is digested with *Nru*I and *Xho*I, generating a DNA fragment which encodes the CMV major immediate early promoter (CMV MIEP), mCCR7 coding sequence, the EMC internal ribosome entry site (IRES), the puromycin resistance gene, and the SV40 polyadenylation signal. The purified *Nru*I-*Xho*I fragment is then cloned into the pGEMm78 vector digested with *Sma*I and *Xho*I. These sites are compatible with the *Nru*I and *Xho*I sites of the mCCR7 fragment for ligation. The resulting construct (pGEMm78IRESmCCR7) contains the m78 gene disrupted by the insertion of the mCCR7 gene and an IRES driven puromycin selection marker.

Please replace the paragraph beginning at page 36, line 30, with the following amended paragraph:

Using viral DNA extracted from human CMV strain AD169 (Genbank Accession no. x17403) virions as template, PCR amplification is carried out using the primers: gcggtaccgcgacgccgtcgctggg (SEQ ID NO:21) (108 up) and- tggatccgtcagggaaatacaag (SEQ ID NO:22) (108 low) to amplify AD108. The resulting 1300 bp fragment is purified, digested with

*Bam*HI and *KpnI*, and cloned into *Bam*HI and *Kpn*I digested vector (pGEM3 (Promega)). The resulting construct is called pGEM108.

Please replace the paragraph beginning at page 37, line 3, with the following amended paragraph:

Using the same viral DNA template as above, PCR amplification is carried out using the primers: atggatcctcttctatcacggtggc (SEQ ID NO:23) -(109 up) and gcggatccaggatcgatttcgtgcg (SEQ ID NO:24) -(109 low) to amplify AD109. The resulting 1085 bp fragment is purified, digested with *Bam*HI, and cloned into pGEM108 cut with *Bam*HI with the end homologous to AD109up juxtaposed to sequence homologous to AD108low. The resulting construct is called pGEM108/109.

Please replace the paragraph beginning at page 37, line 9, with the following amended paragraph:

To clone the Bacillus anthracis protective antigen (BAPA; Genbank Accession no. M22589), DNA is isolated from bacilli containing the BAPA sequence (e.g., pBLSCRPPA from Iacono-Connors L.C. at U.S. Army Medical Research Institute of Infectious Diseases, Frederick MA) by routine means (e.g. using commercially available kits from Qiagen, CA) and used as template for PCR with the primers ggcccggggaagttaaacaggagaaccg (SEQ ID NO:25) (BAPAup) and gggatatcttaccttatcctatctcat (SEQ ID NO:26) (BAPAlow). The resulting 2229 bp product is purified, cut with *Eco*RV and *Xma*I, and cloned into *Eco*RV and *Xma*I-digested vector (Clontech pIREShyg2). The resulting construct is called pBAPAiresHyg.

Please replace the paragraph beginning at page 37, line 18, with the following amended paragraph:

The following complimentary oligo sequences containing the Ig kappa leader sequence (Acc# D84070) are synthesized:

5'-ctagcatggagacagacacactcctgctatgggtactgctgctctgggttccaggttccactggtgaccc-3' (SEQ ID NO:27)

5'-ccgggggtcaccagtggaacctggaacccagagcagcagtacccatagcaggagtgtgtctgtctccatg-3' (SEQ ID NO:28)

and annealed to give a double-stranded oligonucleotide with overhangs for the restriction enzymes NheI and a XmaI. This synthetic sequence is cloned into *Nhe*I and *Xma*I-digested pBAPAiresHyg. The resulting construct is called pSecBAPAiresHyg.

Please replace the paragraph beginning at page 38, line 17, with the following amended paragraph:

Using viral DNA extracted from rhesus CMV (e.g., strain Rh68.1 (ATCC # VR 677)), virions as template, PCR amplification is carried out using the primers: cggaattcctctttagtcggcagggtctt (SEQ ID NO:29) (Rh32up) and ctggatccgtggctttgtctttggctttt (SEQ ID NO:30) (Rh33low) to amplify Rh32/33. The resulting 1404 bp fragment is purified, digested with *Bam*HI and *Eco*RI, and cloned into *Bam*HI and *Eco*RI digested vector (pGEM3 (Promega)). The resulting construct is called pGEM32-33.

Please replace the paragraph beginning at page 38, line 23, with the following amended paragraph:

To clone the Bacillus anthracis protective antigen (BAPA; Genbank Accession no. M22589), DNA is isolated from bacilli containing the BAPA sequence or from a plasmid containing this sequence (e.g., pBLSCRPPA from Iacono-Connors L.C. at U.S. Army Medical Research Institute of Infectious Diseases, Frederick MA) by routine means (e.g. using commercially available kits from Qiagen, CA) and used as template for PCR with the primers

ggcccggggaagttaaacaggagaaccg (SEQ ID NO:25) (BAPAup) and gggatatcttaccttatcctatctcat (SEQ ID NO:26) (BAPAlow). The resulting 2229 bp product is purified, cut with *Eco*RV and *Xma*I, and cloned into *Eco*RV and *Xma*I-digested vector (Clontech pIRESHyg2). The resulting construct is called pBAPAiresHyg.

Please replace the paragraph beginning at page 38, line 32, with the following amended paragraph:

The following complimentary oligo sequences containing the Ig kappa leader sequence (Acc# D84070) are synthesized:

5'-ctagcatggagacagacacactcctgctatgggtactgctgctctgggttccaggttccactggtgaccc-3' (SEQ ID NO:27)

5'-ccgggggtcaccagtggaacctggaacccagagcagcagtacccatagcaggagtgtgtctgtctccatg-3' (SEQ ID NO:28)

and annealed to give a double-stranded oligonucleotide with overhangs for the restriction enzymes *Nhe*I and a *Xma*I. This synthetic sequence is cloned into *Nhe*I and *Xma*I-digested pBAPAiresHyg. The resulting construct is called pSecBAPAiresHyg.

Please replace the paragraph beginning at page 40, line 23, with the following amended paragraph:

The dissemination of $CCR7^+$ and $CCR7^-$ virus or virus infected cells to SLO is determined. Suitable assays for detecting this spread include gross measurements of SLO size or quantitative PCR of viral DNA. In one suitable assay, DNA isolated from SLO (e.g., using commercially available kits from Qiagen, CA) is assayed for viral DNA by PCR using CMV specific primers. For example, in one embodiment, DNA is purified from rhesus macaque SLO, then used as template for nested PCR with primers able to amplify the RhCMV immediate early 2 gene (5' GCC AAT GCA TCC TCT GGA TGT ATT GTG A 3' (SEQ ID NO:31) and 5' TGC

TTG GGG AAT CTC TGC AC 3' (SEQ ID NO:32) then 5' CCC TTC CTG ACT ACT AAT GTA C 3' (SEQ ID NO:33) and 5' TTG GGG AAT CTC TGC ACA AG 3' (SEQ ID NO:34)) (see, e.g., Tarantal -et al., 1998, *J Infect Dis* 177:446-50). An increased titer of viral DNA in SLO tissues of animals infected with CCR7 knock in virus versus controls indicates CCR7 directed migration of virus or virus infected cells to SLO.

Please replace the paragraph beginning at page 43, line 15, with the following amended paragraph:

In another suitable assay, blood is assayed for viral DNA by PCR using CMV specific primers. For example, in one embodiment, DNA is purified from plasma (e.g., using commercially available kits from Qiagen, CA), then used as template for nested PCR with primers able to amplify the RhCMV immediate early 2 gene (5' GCC AAT GCA TCC TCT GGA TGT ATT GTG A 3' (SEQ ID NO:31) and 5' TGC TTG GGG AAT CTC TGC AC 3' (SEQ ID NO:32) then 5' CCC TTC CTG ACT ACT AAT GTA C 3' (SEQ ID NO:33) and 5' TTG GGG AAT CTC TGC ACA AG 3' (SEQ ID NO:34)) (see, e.g., Tarantal -et al., 1998, *J Infect Dis* 177:446-50). Inhibition of CMV dissemination is demonstrated by a difference of viral titer or kinetics (as described *supra*) as assessed by levels of viral DNA in peripheral blood.